

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/588,323
Source: IFWP
Date Processed by STIC: 08/11/2006

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IFWP

RAW SEQUENCE LISTING

DATE: 08/11/2006

PATENT APPLICATION: US/10/588,323

TIME: 11:03:16

Input Set : A:\253780.txt

Output Set: N:\CRF4\08112006\J588323.raw

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3 <110> APPLICANT: Astellas US LLC
4   MAGILAVY, Daniel
6 <120> TITLE OF INVENTION: METHODS OF TREATING SKIN DISORDERS
8 <130> FILE REFERENCE: 253780
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/588,323
C--> 10 <141> CURRENT FILING DATE: 2006-08-03
10 <150> PRIOR APPLICATION NUMBER: 60/542,311
11 <151> PRIOR FILING DATE: 2004-02-06
13 <150> PRIOR APPLICATION NUMBER: PCT/US2005/003907
14 <151> PRIOR FILING DATE: 2005-02-07
16 <160> NUMBER OF SEQ ID NOS: 8
18 <170> SOFTWARE: PatentIn version 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 753
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(750)
30 <220> FEATURE:
31 <221> NAME/KEY: sig_peptide
32 <222> LOCATION: (1)..(84)
34 <220> FEATURE:
35 <221> NAME/KEY: misc_feature
36 <222> LOCATION: (1)..(750)
37 <223> OTHER INFORMATION: "Human transmembrane LFA-3"
39 <220> FEATURE:
40 <221> NAME/KEY: mat_peptide
41 <222> LOCATION: (85)..(750)
43 <220> FEATURE:
44 <221> NAME/KEY: misc_feature
45 <222> LOCATION: (646)..(646)
46 <223> OTHER INFORMATION: "Transmembrane domain"
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51      -25      -20      -15
53 gtc tgc ctg ctg cac tgc ttt ggt ttc atc agc tgt ttt tcc caa caa      96
54 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
55      -10      -5      -1  1
57 ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta cca agc aat      144
58 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
59 5          10          15          20

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61 gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat aaa gtt gca      192
62 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
63              25              30              35
65 gaa ctg gaa aat tct gaa ttc aga gct ttc tca tct ttt aaa aat agg      240
66 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
67              40              45              50
69 gtt tat tta gac act gtg tca ggt agc ctc act atc tac aac tta aca      288
70 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
71              55              60              65
73 tca tca gat gaa gat gag tat gaa atg gaa tcg cca aat att act gat      336
74 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
75              70              75              80
77 acc atg aag ttc ttt ctt tat gtg ctt gag tct ctt cca tct ccc aca      384
78 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
79 85              90              95              100
81 cta act tgt gca ttg act aat gga agc att gaa gtc caa tgc atg ata      432
82 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
83              105              110              115
85 cca gag cat tac aac agc cat cga gga ctt ata atg tac tca tgg gat      480
86 Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
87              120              125              130
89 tgt cct atg gag caa tgt aaa cgt aac tca acc agt ata tat ttt aag      528
90 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
91              135              140              145
93 atg gaa aat gat ctt cca caa aaa ata cag tgt act ctt agc aat cca      576
94 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
95              150              155              160
97 tta ttt aat aca aca tca atc att ttg aca acc tgt atc cca agc      624
98 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
99 165              170              175              180
101 agc ggt cat tca aga cac aga tat gca ctt ata ccc ata cca tta gca      672
102 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
103              185              190              195
105 gta att aca aca tgt att gtg ctg tat atg aat ggt att ctg aaa tgt      720
106 Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile Leu Lys Cys
107              200              205              210
109 gac aga aaa cca gac aga acc aac tcc aat tga      753
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115 <211> LENGTH: 250
116 <212> TYPE: PRT
117 <213> ORGANISM: Homo sapiens
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125 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
126              -10              -5              -1 1
129 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn

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130 5          10          15          20
133 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
134          25          30          35
137 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
138          40          45          50
141 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
142          55          60          65
145 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
146          70          75          80
149 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
150 85          90          95          100
153 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
154          105          110          115
157 Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
158          120          125          130
161 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
162          135          140          145
165 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
166          150          155          160
169 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
170 165          170          175          180
173 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
174          185          190          195
177 Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile Leu Lys Cys
178          200          205          210
181 Asp Arg Lys Pro Asp Arg Thr Asn Ser Asn
182          215          220
185 <210> SEQ ID NO: 3
186 <211> LENGTH: 723
187 <212> TYPE: DNA
188 <213> ORGANISM: Homo sapiens
191 <220> FEATURE:
192 <221> NAME/KEY: CDS
193 <222> LOCATION: (1)..(720)
195 <220> FEATURE:
196 <221> NAME/KEY: sig_peptide
197 <222> LOCATION: (1)..(84)
199 <220> FEATURE:
200 <221> NAME/KEY: misc_feature
201 <222> LOCATION: (1)..(720)
202 <223> OTHER INFORMATION: "Human PI-linked LFA-3"
204 <220> FEATURE:
205 <221> NAME/KEY: mat_peptide
206 <222> LOCATION: (85)..(720)
208 <220> FEATURE:
209 <221> NAME/KEY: misc_feature
210 <222> LOCATION: (568)..(720)
211 <223> OTHER INFORMATION: "signal sequence for PI-linkage"
213 <400> SEQUENCE: 3

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214 atg gtt gct ggg agc gac gcg ggg cgg gcc ctg ggg gtc ctc agc gtg      48
215 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
216          -25          -20          -15
218 gtc tgc ctg ctg cac tgc ttt ggt ttc atc agc tgt ttt tcc caa caa      96
219 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
220          -10          -5          -1  1
222 ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta cca agc aat      144
223 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
224 5          10          15          20
226 gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat aaa gtt gca      192
227 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
228          25          30          35
230 gaa ctg gaa aat tct gaa ttc aga gct ttc tca tct ttt aaa aat agg      240
231 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
232          40          45          50
234 gtt tat tta gac act gtg tca ggt agc ctc act atc tac aac tta aca      288
235 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
236          55          60          65
238 tca tca gat gaa gat gag tat gaa atg gaa tcg cca aat att act gat      336
239 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
240          70          75          80
242 acc atg aag ttc ttt ctt tat gtg ctt gag tct ctt cca tct ccc aca      384
243 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
244 85          90          95          100
246 cta act tgt gca ttg act aat gga agc att gaa gtc caa tgc atg ata      432
247 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
248          105          110          115
250 cca gag cat tac aac agc cat cga gga ctt ata atg tac tca tgg gat      480
251 Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
252          120          125          130
254 tgt cct atg gag caa tgt aaa cgt aac tca acc agt ata tat ttt aag      528
255 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
256          135          140          145
258 atg gaa aat gat ctt cca caa aaa ata cag tgt act ctt agc aat cca      576
259 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
260          150          155          160
262 tta ttt aat aca aca tca tca atc att ttg aca acc tgt atc cca agc      624
263 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
264 165          170          175          180
266 agc ggt cat tca aga cac aga tat gca ctt ata ccc ata cca tta gca      672
267 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
268          185          190          195
270 gta att aca aca tgt att gtg ctg tat atg aat ggt atg tat gct ttt      720
271 Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Met Tyr Ala Phe
272          200          205          210
274 taa      723
277 <210> SEQ ID NO: 4
278 <211> LENGTH: 240
279 <212> TYPE: PRT

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280 <213> ORGANISM: Homo sapiens
282 <400> SEQUENCE: 4
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289           -10                      -5                      -1  1
292 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
293 5              10              15              20
296 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
297           25              30              35
300 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
301           40              45              50
304 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
305           55              60              65
308 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
309           70              75              80
312 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
313 85              90              95              100
316 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
317           105             110             115
320 Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
321           120             125             130
324 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
325           135             140             145
328 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
329           150             155             160
332 Leu Phe Asn Thr Thr Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
333 165             170             175             180
336 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
337           185             190             195
340 Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Met Tyr Ala Phe
341           200             205             210
344 <210> SEQ ID NO: 5
345 <211> LENGTH: 1056
346 <212> TYPE: DNA
347 <213> ORGANISM: Homo sapiens
350 <220> FEATURE:
351 <221> NAME/KEY: CDS
352 <222> LOCATION: (1)..(1053)
354 <220> FEATURE:
355 <221> NAME/KEY: sig_peptide
356 <222> LOCATION: (1)..(72)
358 <220> FEATURE:
359 <221> NAME/KEY: misc_feature
360 <222> LOCATION: (1)..(1053)
361 <223> OTHER INFORMATION: "Human CD2"
363 <220> FEATURE:
364 <221> NAME/KEY: mat_peptide
365 <222> LOCATION: (73)..(1053)

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VERIFICATION SUMMARY

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TIME: 11:03:17

Input Set : A:\253780.txt

Output Set: N:\CRF4\08112006\J588323.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date